

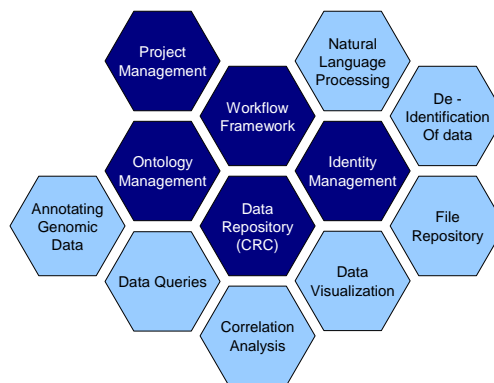
THE i2b2 HIVE: A SOFTWARE ARCHITECTURE FOR THE CLINICAL RESEARCH CHART

Chueh, Henry C.¹; Berkowicz, David A.¹; Murphy, Shawn N.¹; Kohane, Isaac²
¹Massachusetts General Hospital, Boston, MA; ²Children's Hospital, Boston, MA

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A key goal of i2b2 is to develop methods for systematically collecting and managing clinical research data over time into a modern-day clinical research chart. As with clinical systems, software tools and applications will play an increasing large role in this activity. Unlike clinical systems, the diversity of research practice and its rapidly changing landscape suggests that any particular software suite will likely face early obsolescence. The i2b2 hive is a software architecture intended to promote a scalable model for continuous development of software components that can service the clinical research chart.

The i2b2 hive can be described as a collection of Web services, or “cells”, that are aggregated to perform a variety of tasks with data from the clinical research chart. Each cell can define a functional component that can be developed independently from other cells, and describes a public software interface minimally as XML over HTTP, and optionally supports a standard for a managed user interface. By leveraging the network for functional messaging, this approach allows free reuse of existing services to be combined into new functional services and cells -- not unlike the “mash up” programming that is emerging autonomously on the Web. The i2b2 team is developing reference implementations of cells to handle core functions such as repository, workflow, identity, project, and ontology management.



The implementation of an i2b2 cell is intentionally simple since the i2b2 hive is broadly inclusive of diverse software development methodologies, languages, and most importantly, researchers who are not expert software engineers but who have developed valuable software services. The i2b2 cell protocol defines basic mechanisms to support authentication, session information, simple routing, and callback notifications, all as part of the i2b2 XML schema for messaging. Support for managing transmission of relationships between de-identified patients and their related clinical research data is included.

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